

## SEQUENCE LISTING

<110> Keler, Tibor  
Deo, Yashwant

<120> HUMAN MONOCLONAL ANTIBODIES TO HER2/NEU

<130> MXI-160US

<140> US 10/031,722

<141> 2002-01-18

<150> PCT/US00/20272

<151> 2000-07-25

<150> US 60/146,313

<151> 1999-07-29

<150> US 60/188,539

<151> 2000-03-10

<160> 13

<170> PatentIn Ver. 2.0

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Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	
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gcc	atg	acc	tgg	gtc	cgc	cag	gct	cca	ggg	aag	ggg	ctg	gag	tgg	gtc	144
Ala	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
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tca	gct	atc	agt	ggt	agt	ggt	tat	agc	aca	tac	tac	gca	gac	tcc	gag	192
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Tyr	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Glu	
	50					55					60					
aag	ggc	cgg	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	acg	ctg	tat	240
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70				75					80		
ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gcc	gta	tat	tac	tgt	288
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90						95		
gcg	aaa	ggg	ttt	cag	tat	ggt	tcg	ggg	agt	tat	tat	acc	cac	ttt	gac	336
Ala	Lys	Gly	Phe	Gln	Tyr	Gly	Ser	Gly	Ser	Tyr	Tyr	Thr	His	Phe	Asp	

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115	120		

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 35 40 45  
 Ser Ala Ile Ser Gly Ser Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Glu  
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 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
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 gac aga gtc acc atc act tgt cgg gcg agt cag ggt att agc agc tgg 96  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
 20 25 30  
 tta gcc tgg tat cag cag aaa cca gag aaa gcc cct aag tcc ctg atc 144  
 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile  
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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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gaa gat ttt gca act tat tac tgc caa cag tat aat agt tac ccg tac 288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr
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Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                55                60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
    65                70                75                80

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Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35                      40                      45

gca gta ata tgg tat gat ggc agt aat aaa tac cat gca gac tcc gtg   192
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr His Ala Asp Ser Val
      50                      55                      60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat   240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65                      70                      75                      80

ctg caa atg aac agt ctg aga gcc gag gac acg gct gtg tat tac tgt   288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
      85                      90                      95

gcg aga aac tat ggt ttg ggg agt tat tat aac tac ttt gac ttc tgg   336
Ala Arg Asn Tyr Gly Leu Gly Ser Tyr Tyr Asn Tyr Phe Asp Phe Trp
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Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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 <213> Homo sapiens

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Asp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35                      40                      45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr His Ala Asp Ser Val
      50                      55                      60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65                      70                      75                      80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
      85                      90                      95

Ala Arg Asn Tyr Gly Leu Gly Ser Tyr Tyr Asn Tyr Phe Asp Phe Trp
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Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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gac aga gtc acc atc act tgt cgg gcg agt cat ggt att agc agc tgg	96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Gly Ile Ser Ser Trp	
20 25 30	
tta gcc tgg tat cag cag aaa cca gag aaa gcc cct aag tcc ctg atc	144
Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile	
35 40 45	
tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc	192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly	
50 55 60	
agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	
65 70 75 80	
gaa gat ttt gca act tat tac tgc caa cag tat aat agt tac ccg tac	288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr	
85 90 95	
act ttt ggc cag ggg acc aag ctg gag atc aaa	321
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys	
100 105	

<210> 8  
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 <212> PRT  
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35 40 45	
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly	
50 55 60	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	
65 70 75 80	
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Tyr	

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90

95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
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 tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt agc tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30  
 gtc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144  
 Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 gca gtt ata tgg tat gat gga agt aat aaa tac tat gca gac tcc gtg 192  
 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 gcg ctt atg gtt cgg gga ctt att ata acg ggg tac ttt gac tac tgg 336  
 Ala Leu Met Val Arg Gly Leu Ile Ile Thr Gly Tyr Phe Asp Tyr Trp  
 100 105 110  
 ggc cag gga acc ctg gtc acc gtc tcc tca 366  
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 115 120

<210> 10  
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val  
           50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
       65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                  90                  95

Ala Leu Met Val Arg Gly Leu Ile Ile Thr Gly Tyr Phe Asp Tyr Trp  
                   100                  105                  110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
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gaa aga gcc acc ctg tcc tgc agg gcc agt cag agt gtt agc agc tac 96  
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr  
           20                  25                  30

tta gcc tgg tac caa cag aaa cct ggc cag gct ccc agg ctg ctg atc 144  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
           35                  40                  45

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc 192  
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
           50                  55                  60

agt ggg tct ggg aca gac ttc act ctg acc atc agc agc cta gag cct 240  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
       65                  70                  75                  80

gaa gat ttt gca gtt tat tac tgt cag cag cgt agc aac tgg cct ccg 288  
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
                   85                  90                  95

tac act ttt ggc cag ggg acc aag ctg gag atc aaa 324  
 Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
 85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 100 105

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&lt;211&gt; 3159

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: cloning vector

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